

substantially invade cells of a host, and cannot spread substantially within infected cells and from infected to uninfected cells of the host, and cannot produce toxins that will kill substantial numbers of the host's infected, as well as uninfected, cells, wherein the modified wild strain is selected from the group consisting of:

- (A) a wild strain of *Shigella*, the genome of which is modified so that a first gene, coding for a protein necessary for the wild strain of *Shigella* to invade cells, as well as tissues, of the host, and a second gene, coding for a protein necessary for the wild strain of *Shigella* to spread within infected cells and between infected and uninfected cells of the host, are wholly or partly removed or permanently inactivated, wherein the *Shigella* is an *S. flexneri* and the first gene codes for the production or use of aerobactin by the *S. flexneri* and the second gene codes for intra- or intercellular spread; and
- (B) a wild strain of *Shigella*, the genome of which is modified so that a first gene, coding for a protein necessary for the wild strain of *Shigella* to invade cells, as well as tissues, of the host, and a second gene, coding for a protein necessary for the wild strain of *Shigella* to spread within infected cells and between infected and uninfected cells of the host, are wholly or partly removed or permanently inactivated, in which the *Shigella* is an *S. dysenteriae* 1, the genome of which is modified so that a third gene, coding for the production or use of